

A-m Baker

1632 #10  
4/21/99  
amb

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/866,279A

DATE: 04/21/1999  
TIME: 14:02:37

INPUT SET: S31553.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1  
2  
3 (1) General Information:  
4 (i) APPLICANT: Susan DYMECKI  
5 (ii) TITLE OF INVENTION: Use of F1p Recombinase in Mice  
6 (iii) NUMBER OF SEQUENCES: 23  
7 (iv) CORRESPONDENCE ADDRESS:  
8 (A) ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
9 (B) STREET: 1100 New York Avenue, N.W.  
10 (C) CITY: Washington  
11 (D) STATE: D.C.  
12 (E) COUNTRY: USA  
13 (F) ZIP: 20005-3918  
14 (v) COMPUTER READABLE FORM:  
15 (A) MEDIUM TYPE: Floppy disk  
16 (B) COMPUTER: IBM PC compatible  
17 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
18 (D) SOFTWARE: Microsoft Word  
19 (vi) CURRENT APPLICATION DATA:  
20 (A) APPLICATION NUMBER: US 08/866,279  
21 (B) FILING DATE: 30-MAY-1997  
22 (C) CLASSIFICATION:  
23  
24 (2) INFORMATION FOR SEQ ID NO:1:  
25 (i) SEQUENCE CHARACTERISTICS:  
26 (A) LENGTH: 79 base pairs  
27 (B) TYPE: nucleic acid  
28 (C) STRANDEDNESS: single  
29 (D) TOPOLOGY: linear  
30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
31 CCGGTGAAGT TCCTATTCCG AAGTTCCTAT TCTCTAGAAA GTATAGGAAC 50  
32 TTCCCTAGGA GATCTTCGAA GGCTCGAGC 79  
33  
34 (2) INFORMATION FOR SEQ ID NO:2:  
35 (i) SEQUENCE CHARACTERISTICS:  
36 (A) LENGTH: 59 base pairs  
37 (B) TYPE: nucleic acid  
38 (C) STRANDEDNESS: single  
39 (D) TOPOLOGY: linear  
40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
41 TAGCTACGTA GAAGTTCCTA TTCCGAAGTT CCTATTCTCT AGAAAGTATA 50  
42 GGAAGTCA 59  
43  
44 (2) INFORMATION FOR SEQ ID NO:3:  
45 (i) SEQUENCE CHARACTERISTICS:  
46 (A) LENGTH: 54 base pairs

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47 (B) TYPE: nucleic acid  
48 (C) STRANDEDNESS: single  
49 (D) TOPOLOGY: linear  
50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
51 CTAGGGAAGT TCCTATACTT TCTAGAGAAT AGGAACTTCG GAATAGGAAC 50  
52 TTCA 54  
53  
54 (2) INFORMATION FOR SEQ ID NO:4:  
55 (i) SEQUENCE CHARACTERISTICS:  
56 (A) LENGTH: 84 base pairs  
57 (B) TYPE: nucleic acid  
58 (C) STRANDEDNESS: single  
59 (D) TOPOLOGY: linear  
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
61 CCGGTGAAGT TCCTATACTT TCTAGAGAAT AGGAACTTCG GAATAGGAAC 50  
62 TTCTACGTAG CTAGCTCGAG CCTTCGAAGA TCTC 84  
63  
64 (2) INFORMATION FOR SEQ ID NO:5:  
65 (i) SEQUENCE CHARACTERISTICS:  
66 (A) LENGTH: 23 base pairs  
67 (B) TYPE: nucleic acid  
68 (C) STRANDEDNESS: single  
69 (D) TOPOLOGY: linear  
70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
71 GTAAGGTACC GGTGAAGTTC CTA 23  
72  
73 (2) INFORMATION FOR SEQ ID NO:6:  
74 (i) SEQUENCE CHARACTERISTICS:  
75 (A) LENGTH: 23 base pairs  
76 (B) TYPE: nucleic acid  
77 (C) STRANDEDNESS: single  
78 (D) TOPOLOGY: linear  
79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
80 TTCAACCCACC GGTGAAGTTC CTA 23  
81  
82 (2) INFORMATION FOR SEQ ID NO:7:  
83 (i) SEQUENCE CHARACTERISTICS:  
84 (A) LENGTH: 211 base pairs  
85 (B) TYPE: nucleic acid  
86 (C) STRANDEDNESS: single  
87 (D) TOPOLOGY: linear  
88 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
89 GGTACCGAGC TCAGCCACCA TGAAGTCTCC AAAGAAGAAG CGTAAGGTAC 50  
90 CCGGTGAAGTT CCTATTCCGA AGTTCCTATT CTCTAGAAAG TATAGGAACT 100  
91 TCACCGGTGG GTGAAGACCA GAAACAGCAC CTCGAACTGA GCCGCGATAT 150  
92 TGCCAGCGT TTCAACGCGC TGTATGGCGA GATCGATCCC GTCGTTTTAC 200  
93 AACGTCGTGA C 211  
94  
95 (2) INFORMATION FOR SEQ ID NO:8:  
96 (i) SEQUENCE CHARACTERISTICS:  
97 (A) LENGTH: 64 amino acids  
98 (B) TYPE: amino acid  
99 (C) STRANDEDNESS: single

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100      (D) TOPOLOGY: linear
101  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
102  Met Thr Ala Pro Lys Lys Lys Arg Lys Val Pro Val Lys Phe Leu
103  1          5          10          15
104  Phe Arg Ser Ser Tyr Ser Leu Glu Ser Ile Gly Thr Ser Pro Val
105          20          25          30
106  Gly Glu Asp Gln Lys Gln His Leu Glu Leu Ser Arg Asp Ile Ala
107          35          40          45
108  Gln Arg Phe Asn Ala Leu Tyr Gly Glu Ile Asp Pro Val Val Leu
109          50          55          60
110  Gln Arg Arg Asp
111
112  (2) INFORMATION FOR SEQ ID NO:9:
113      (i) SEQUENCE CHARACTERISTICS:
114          (A) LENGTH: 8 amino acids
115          (B) TYPE: amino acid
116          (C) STRANDEDNESS: single
117          (D) TOPOLOGY: linear
118  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
119  Ala Pro Lys Lys Lys Arg Lys Val
120  1          5
121
122  (2) INFORMATION FOR SEQ ID NO:10:
123      (i) SEQUENCE CHARACTERISTICS:
124          (A) LENGTH: 16 amino acids
125          (B) TYPE: amino acid
126          (C) STRANDEDNESS: single
127          (D) TOPOLOGY: linear
128  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
129  Lys Phe Leu Phe Arg Ser Ser Tyr Ser Leu Glu Ser Ile Gly Thr
130  1          5          10          15
131  Ser
132
133  (2) INFORMATION FOR SEQ ID NO:11:
134      (i) SEQUENCE CHARACTERISTICS:
135          (A) LENGTH: 27 amino acids
136          (B) TYPE: amino acid
137          (C) STRANDEDNESS: single
138          (D) TOPOLOGY: linear
139  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
140  Pro Val Gly Glu Asp Gln Lys Gln His Leu Glu Leu Ser Arg Asp
141  1          5          10          15
142  Ile Ala Gln Arg Phe Asn Ala Leu Tyr Gly Glu Ile
143          20          25
144
145  (2) INFORMATION FOR SEQ ID NO:12:
146      (i) SEQUENCE CHARACTERISTICS:
147          (A) LENGTH: 13 base pairs
148          (B) TYPE: nucleic acid
149          (C) STRANDEDNESS: single
150          (D) TOPOLOGY: linear
151  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
152  GAAGTTCCTA TTC

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153  
154 (2) INFORMATION FOR SEQ ID NO:13:  
155 (i) SEQUENCE CHARACTERISTICS:  
156 (A) LENGTH: 13 base pairs  
157 (B) TYPE: nucleic acid  
158 (C) STRANDEDNESS: single  
159 (D) TOPOLOGY: linear  
160 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:  
161 GAAGTTCCTA TAC 13  
162  
163 (2) INFORMATION FOR SEQ ID NO:14:  
164 (i) SEQUENCE CHARACTERISTICS:  
165 (A) LENGTH: 34 base pairs  
166 (B) TYPE: nucleic acid  
167 (C) STRANDEDNESS: single  
168 (D) TOPOLOGY: linear  
169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  
170 GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTC 34  
171  
172 (2) INFORMATION FOR SEQ ID NO:15:  
173 (i) SEQUENCE CHARACTERISTICS:  
174 (A) LENGTH: 48 base pairs  
175 (B) TYPE: nucleic acid  
176 (C) STRANDEDNESS: single  
177 (D) TOPOLOGY: linear  
178 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  
179 GAAGTTCCTA TTCCGAAGTT CCTATTCTCT AGAAAGTATA GGAAGTTC 48  
180  
181 (2) INFORMATION FOR SEQ ID NO:16:  
182 (i) SEQUENCE CHARACTERISTICS:  
183 (A) LENGTH: 1272 base pairs  
184 (B) TYPE: nucleic acid  
185 (C) STRANDEDNESS: single  
186 (D) TOPOLOGY: linear  
187 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:  
188 ATGCCACAAT TTGATATATT ATGTAAAACA CCACCTAAGG TGCTTGTTCTG TCAGTTTGTG 60  
189 GAAAGGTTTG AAAGACCTTC AGGTGAGAAA ATAGCATTAT GTGCTGCTGA ACTAACCTAT 120  
190 TTATGTTGGA TGATTACACA TAACGGAACA GCAATCAAGA GAGCCACATT CATGAGCTAT 180  
191 AATACTATCA TAAGCAATTC GCTGAGTTTG GATATTGTCA ACAAGTCACT GCAGTTTAAA 240  
192 TACAAGACGC AAAAAGCAAC AATTCTGGAA GCCTCATTA AGAAATTGAT TCCTGCTTGG 300  
193 GAATTTACAA TTATTCCTTA CTATGGACAA AACATCAAT CTGATATCAC TGATATTGTA 360  
194 AGTAGTTTGC AATTACAGTT CGAATCATCG GAAGAAGCAG ATAAGGGAAA TAGCCACAGT 420  
195 AAAAAAATGC TTAAAGCACT TCTAAGTGAG GGTGAAAGCA TCTGGGAGAT CACTGAGAAA 480  
196 ATACTAAATT CGTTTGAGTA TACTTCGAGA TTTACAAAAA CAAAAACTTT ATACCAATTC 540  
197 CTCTTCCTAG CTACTTTCAT CAATTGTGGA AGATTCAGCG ATATTAAGAA CGTTGATCCG 600  
198 AAATCATTTA AATTAGTCCA AAATAAGTAT CTGGGAGTAA TAATCCAGTG TTTAGTGACA 660  
199 GAGACAAAGA CAAGCGTTAG TAGGCACATA TACTTCTTTA GCGCAAGGGG TAGGATCGAT 720  
200 CCACTTGTAT ATTTGGATGA ATTTTGGAGG AATTCTGAAC CAGTCCTAAA ACGAGTAAAT 780  
201 AGGACCGGCA ATTCCTCAAG CAACAAGCAG GAATACCAAT TATTAAGA TAAGTATGTC 840  
202 AGATCGTACA ACAAGCTTT GAAGAAAAAT GCGCCTTATT CAATCTTGC TATAAAAAAT 900  
203 GGCCCAAAAT CTCACATTGG AAGACATTGG ATGACCTCAT TTCTTTCAAT GAAGGGCCTA 960  
204 ACGGAGTTGA CTAATGTTGT GGGAAATTGG AGCGATAAGC GTGCTTCTGC CGTGGCCAGG 1020  
205 ACAACGTATA CTCATCAGAT AACAGCAATA CCTGATCACT ACTTCGCACT AGTTTCTCGG 1080

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206 TACTATGCAT ATGATCCAAT ATCAAAGGAA ATGATAGCAT TGAAGGATGA GACTAATCCA 1140  
207 ATTGAGGAGT GGCAGCATAT AGAACAGCTA AAGGGTAGTG CTGAAGGAAG CATACGATAC 1200  
208 CCCGCATGGA ATGGGATAAT ATCACAGGAG GTACTAGACT ACCTTTCATC CTACATAAAT 1260  
209 AGACGCATAT AA 1272

210

211 (2) INFORMATION FOR SEQ ID NO:17:

212 (i) SEQUENCE CHARACTERISTICS:

213 (A) LENGTH: 423 amino acids

214 (B) TYPE: amino acid

215 (C) STRANDEDNESS: single

216 (D) TOPOLOGY: linear

217 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

218	Met	Pro	Gln	Phe	Asp	Ile	Leu	Cys	Lys	Thr	Pro	Pro	Lys	Val	Leu
219	1				5					10					15
220	Val	Arg	Gln	Phe	Val	Glu	Arg	Phe	Glu	Arg	Pro	Ser	Gly	Glu	Lys
221					20					25					30
222	Ile	Ala	Leu	Cys	Ala	Ala	Glu	Leu	Thr	Tyr	Leu	Cys	Trp	Met	Ile
223					35					40					45
224	Thr	His	Asn	Gly	Thr	Ala	Ile	Lys	Arg	Ala	Thr	Phe	Met	Ser	Tyr
225					50					55					60
226	Asn	Thr	Ile	Ile	Ser	Asn	Ser	Leu	Ser	Leu	Asp	Ile	Val	Asn	Lys
227					65					70					75
228	Ser	Leu	Gln	Phe	Lys	Tyr	Lys	Thr	Gln	Lys	Ala	Thr	Ile	Leu	Glu
229					80					85					90
230	Ala	Ser	Leu	Lys	Lys	Leu	Ile	Pro	Ala	Trp	Glu	Phe	Thr	Ile	Ile
231					95					100					105
232	Pro	Tyr	Tyr	Gly	Gln	Lys	His	Gln	Ser	Asp	Ile	Thr	Asp	Ile	Val
233					110					115					120
234	Ser	Ser	Leu	Gln	Leu	Gln	Phe	Glu	Ser	Ser	Glu	Glu	Ala	Asp	Lys
235					125					130					135
236	Gly	Asn	Ser	His	Ser	Lys	Lys	Met	Leu	Lys	Ala	Leu	Leu	Ser	Glu
237					140					145					150
238	Gly	Glu	Ser	Ile	Trp	Glu	Ile	Thr	Glu	Lys	Ile	Leu	Asn	Ser	Phe
239					155					160					165
240	Glu	Tyr	Thr	Ser	Arg	Phe	Thr	Lys	Thr	Lys	Thr	Leu	Tyr	Gln	Phe
241					170					175					180
242	Leu	Phe	Leu	Ala	Thr	Phe	Ile	Asn	Cys	Gly	Arg	Phe	Ser	Asp	Ile
243					185					190					195
244	Lys	Asn	Val	Asp	Pro	Lys	Ser	Phe	Lys	Leu	Val	Gln	Asn	Lys	Tyr
245					200					205					210
246	Leu	Gly	Val	Ile	Ile	Gln	Cys	Leu	Val	Thr	Glu	Thr	Lys	Thr	Ser
247					215					220					225
248	Val	Ser	Arg	His	Ile	Tyr	Phe	Phe	Ser	Ala	Arg	Gly	Arg	Ile	Asp
249					230					235					240
250	Pro	Leu	Val	Tyr	Leu	Asp	Glu	Phe	Leu	Arg	Asn	Ser	Glu	Pro	Val
251					245					250					255
252	Leu	Lys	Arg	Val	Asn	Arg	Thr	Gln	Asn	Ser	Ser	Ser	Asn	Lys	Gln
253					260					265					270
254	Glu	Tyr	Gln	Leu	Leu	Lys	Asp	Asn	Leu	Val	Arg	Ser	Tyr	Asn	Lys
255					275					280					285
256	Ala	Leu	Lys	Lys	Asn	Ala	Pro	Tyr	Ser	Ile	Phe	Ala	Ile	Lys	Asn
257					290					295					300
258	Gly	Pro	Lys	Ser	His	Ile	Gly	Arg	His	Leu	Met	Thr	Ser	Phe	Leu

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/866,279A**

DATE: 04/21/1999  
TIME: 14:02:39

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Line	Error	Original Text
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